NCBI   results of BLAST

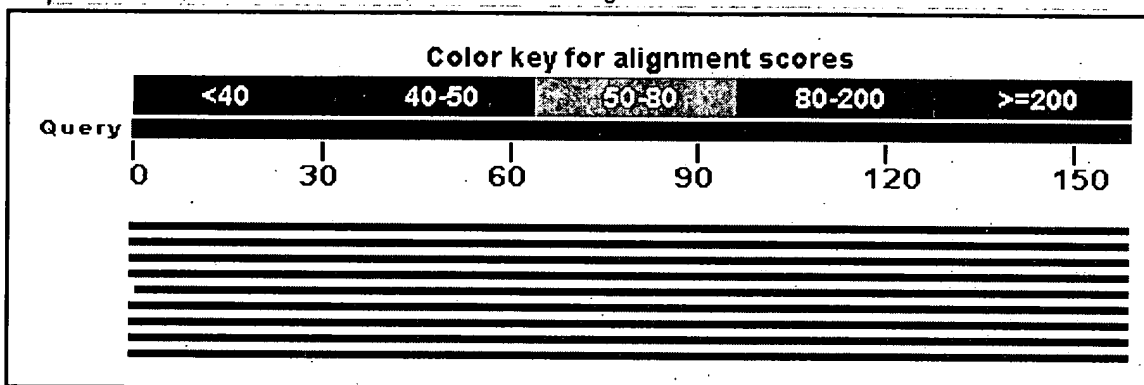## BLASTN 2.2.15 [Oct-15-2006]

RID: 1167425726-9360-210999924966.BLASTQ1

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
4,720,951 sequences; 18,839,166,270 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**
Taxonomy reports

Query=
Length=158

Distribution of 9 Blast Hits on the Query Sequence

Mouse over to see the defline, click to show alignments

Distance tree of results NEW!

Legend for links to other resources: U UniGene E GEO G Gene S Structure M M

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Tot score	Query coverage	v
AY119786.1	Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase	292	292	100%	2
AY251790.1	Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase	287	287	100%	8
AY154881.1	Karenia brevis strain Charlotte Harbor C2 ribulose-1,5-bisphosphate	287	287	100%	8
AY154879.1	Karenia brevis strain Mexico Beach C5 ribulose-1,5-bisphosphate	287	287	100%	8
AY154878.1	Karenia brevis strain Charlotte Harbor A2 ribulose-1,5-bisphosphate	285	285	99%	3
AY154882.1	Karenia brevis strain Piney Island A9 ribulose-1,5-bisphosphate	281	281	100%	4

	gene for plastid product				
AY154880.1	Karenia brevis strain Piney Island B4 ribulose-1,5-bisphosphate	281	281	100%	4
AY154883.1	Karenia brevis strain Mexico Beach B3 ribulose-1,5-bisphosphate	276	276	100%	2
AY154877.1	Karenia brevis strain Appalachicola C6 ribulose-1,5-bisphosphate	276	276	100%	2

Alignments

Get selected sequences	Select all	Deselect all	Distance tree of results

> ☐ gb|AY119786.1| Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase
(rbcL) gene, partial cds; chloroplast gene for chloroplast
product
Length=907

 Score = 292 bits (158), Expect = 2e-76
 Identities = 158/158 (100%), Gaps = 0/158 (0%)
 Strand=Plus/Plus

```
Query  1    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  298  GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT  357

Query  61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  358  ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT  417

Query  121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC  158
            ||||||||||||||||||||||||||||||||||||||
Sbjct  418  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC  455
```

> ☐ gb|AY251790.1| Karenia brevis ribulose-1,5-bisphosphate carboxylase/oxygenase
large subunit (rbcL) mRNA, partial cds; chloroplast gene for
chloroplast product
Length=553

 Score = 287 bits (155), Expect = 8e-75
 Identities = 157/158 (99%), Gaps = 0/158 (0%)
 Strand=Plus/Plus

```
Query  1    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT  60
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT  60

Query  61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT  120

Query  121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC  158
            ||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC  158
```

> ☐ gb|AY154881.1| Karenia brevis strain Charlotte Harbor C2 ribulose-1,5-bisphospha
carboxylase/oxygenase large subunit (rbcL) gene, partial

cds; plastid gene for plastid product
Length=553

 Score = 287 bits (155), Expect = 8e-75
 Identities = 157/158 (99%), Gaps = 0/158 (0%)
 Strand=Plus/Plus

Query 1   GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
            ||||||||||||||||||||||||||||||||||||||
Sbjct 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158

>[gb|AY154879.1| Karenia brevis strain Mexico Beach C5 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

 Score = 287 bits (155), Expect = 8e-75
 Identities = 157/158 (99%), Gaps = 0/158 (0%)
 Strand=Plus/Plus

Query 1   GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct 1   GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT 60

Query 61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT 120

Query 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158
            ||||||||||||||||||||||||||||||||||||||
Sbjct 121 GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC 158

>[gb|AY154878.1| Karenia brevis strain Charlotte Harbor A2 ribulose-1,5-bisphospha
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

 Score = 285 bits (154), Expect = 3e-74
 Identities = 156/157 (99%), Gaps = 0/157 (0%)
 Strand=Plus/Plus

Query 2   ATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCTA 61
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct 2   ATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCTA 61

Query 62   TGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAATG 121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 62   TGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAATG 121

```
Query  122   TCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
             |||||||||||||||||||||||||||||||||||||
Sbjct  122   TCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
```

>☐ gb|AY154882.1| Karenia brevis strain Piney Island A9 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

  Score = 281 bits (152), Expect = 4e-73
  Identities = 156/158 (98%), Gaps = 0/158 (0%)
  Strand=Plus/Plus

```
Query   1    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60
             ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GATGATGAAAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60

Query   61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120

Query   121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
             ||||||| ||||||||||||||||||||||||||||||
Sbjct   121  GTCACGACAGCGACGATGGAAGACATGTATGAAAGAGC   158
```

>☐ gb|AY154880.1| Karenia brevis strain Piney Island B4 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

  Score = 281 bits (152), Expect = 4e-73
  Identities = 156/158 (98%), Gaps = 0/158 (0%)
  Strand=Plus/Plus

```
Query   1    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60
             ||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct   1    GATGATGAGAATATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60

Query   61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61   ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120

Query   121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
             ||||||||||||||||||||||||||||||||||||||
Sbjct   121  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
```

>☐ gb|AY154883.1| Karenia brevis strain Mexico Beach B3 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

  Score = 276 bits (149), Expect = 2e-71
  Identities = 155/158 (98%), Gaps = 0/158 (0%)
  Strand=Plus/Plus

```
Query   1    GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60
```

```
               ||||||||| || ||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct   1      GATGATGAGAACATTAACTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60

Query   61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120

Query   121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
               ||||||||||||||||||||||||||||||||||||||
Sbjct   121 .  GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
```

> □ gb|AY154877.1| Karenia brevis strain Appalachicola C6 ribulose-1,5-bisphosphate
carboxylase/oxygenase large subunit (rbcL) gene, partial
cds; plastid gene for plastid product
Length=553

 Score = 276 bits (149),   Expect = 2e-71
 Identities = 155/158 (98%), Gaps = 0/158 (0%)
 Strand=Plus/Plus

```
Query   1      GATGATGAAAATATTAATTCGCAGCCTTTTATGCGGTATCGTGAACGTTTCCTATACTCT   60
               |||||||| ||||||||| ||||||||||||| |||||||||||||||||||||||||||
Sbjct   1      GATGATGAGAATATTAACTCGCAGCCTTTTACGCGGTATCGTGAACGTTTCCTATACTCT   60

Query   61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   61     ATGGAAGGTGTCAATCATGCTGCCGCAAAAACCGGTGAAATCAAAGGACATTATTTAAAT   120

Query   121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
               ||||||||||||||||||||||||||||||||||||||
Sbjct   121    GTCACGGCAGCGACGATGGAAGACATGTATGAAAGAGC   158
```

[Get selected sequences]   [Select all]   [Deselect all]   [Distance tree of results]

  Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental
samples or phase 0, 1 or 2 HTGS sequences)
    Posted date: Dec 28, 2006 5:47 PM
  Number of letters in database: 1,659,297,086
  Number of sequences in database: 4,720,951
Lambda   K   H
   1.33   0.621   1.12
Gapped
Lambda   K   H
   1.33   0.621   1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 4720951
Number of Hits to DB: 576928
Number of extensions: 2
Number of successful extensions: 2
Number of sequences better than 10: 2
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Length of query: 158

```
Length of database: 18839166270
Length adjustment: 30
Effective length of query: 128
Effective length of database: 18697537740
Effective search space: 2393284830720
Effective search space used: 2393284830720
A: 0
X1: 13 (25.0 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 13 (25.1 bits)
S2: 20 (38.1 bits)
```

NCBI   *results of* **BLAST**

BLASTN 2.2.15 [Oct-15-2006]

RID: 1167424902-29846-208565337440.BLASTQ1

Database: GenBank non-mouse and non-human EST entries
         27,698,245 sequences; 15,888,380,909 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Query=
Length=158

No significant similarity found. For reasons why, **click here**.

   Database: GenBank non-mouse and non-human EST entries
      Posted date: Dec 27, 2006 6:00 PM
   Number of letters in database: -1,291,488,271
   Number of sequences in database: 27,698,245
Lambda   K   H
     1.33   0.621   1.12
Gapped
Lambda   K   H
     1.33   0.621   1.12
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 27698245
Number of Hits to DB: 456698
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 158
Length of database: 15888380909
Length adjustment: 30
Effective length of query: 128
Effective length of database: 15057433559
Effective search space: 1927351495552
Effective search space used: 1927351495552
A: 0
X1: 12 (23.1 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 20 (38.1 bits)